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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/993,308

DATE: 03/06/2002 R-5  
 TIME: 12:44:52

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3 <110> APPLICANT: Gordon-Kamm, William J.  
 4 Lowe, Keith S.  
 5 Larkins, Brian A.  
 6 Dilkes, Brian R.  
 7 Sun, Yuejin  
 9 <120> TITLE OF INVENTION: Cell Cycle Nucleic Acids, Polypeptides and Uses Thereof  
 11 <130> FILE REFERENCE: 1146  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/993,308  
 14 <141> CURRENT FILING DATE: 2001-11-06  
 16 <150> PRIOR APPLICATION NUMBER: 60/246,349  
 17 <151> PRIOR FILING DATE: 2000-11-07  
 19 <160> NUMBER OF SEQ ID NOS: 6  
 21 <170> SOFTWARE: PatentIn version 3.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1372  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Zea mays  
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 29 <221> NAME/KEY: CDS  
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 40 Met Gly Lys Tyr Met Arg Lys Cys Arg Gly Ala Ala  
 41 1 5 10  
 43 ggc gcg gag gtc gcc gcc gtc gag gtt acg cag gtc gtc ggc gtc cgg 217  
 44 Gly Ala Glu Val Ala Ala Val Glu Val Thr Gln Val Val Gly Val Arg  
 45 15 20 25  
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 48 Thr Arg Ser Arg Ser Ala Ala Ala Thr Gly Gly Val Ala Lys Val Ala  
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 51 ccg agg agg aag agg gcg ccg gcg ggg gag cct gct gcc gcc gtg agc 313  
 52 Pro Arg Arg Lys Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser  
 53 45 50 55 60  
 55 gct ggt ggg gac gcc gga agc tgc tac atc cac ctg cgt agc cgc atg 361  
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 60 Leu Phe Met Ala Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro  
 61 80 85 90  
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68 Leu Ala Ala Gly Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn
69      110          115          120
71 ttg ggc ttg ggg ggt cag cgc ggg agc cac acc tgc cgc tcc tac gac      553
72 Leu Gly Leu Gly Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp
73 125          130          135          140
75 gct gca gag gct ggc ggg gat cac gtc ctg gtg gat gtc tcg gcg gcg      601
76 Ala Ala Glu Ala Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala
77          145          150          155
79 agc aac tcc ggg agc ggc cca gac cgc gag agg cga gag acg acg cca      649
80 Ser Asn Ser Gly Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro
81          160          165          170
83 tcg agc cgg gcg cac ggc gag ctc agc gat ctg gag tcg gat ctg gcg      697
84 Ser Ser Arg Ala His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala
85      175          180          185
87 ggg cac aag act ggc ccg tcg cta ccg gcg gca acg ccg gct gcg gag      745
88 Gly His Lys Thr Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu
89      190          195          200
91 ctg atc gtg ccg cca gca cac gag atc cag gag ttc ttc gcc gcc gcc      793
92 Leu Ile Val Pro Pro Ala His Glu Ile Gln Glu Phe Phe Ala Ala Ala
93 205          210          215          220
95 gag gcg gcc cag gcc aag cgc ttt gct tcc aag tac aac ttc gac ttc      841
96 Glu Ala Ala Gln Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe
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99 gtc cgc ggc gtg ccc ctc gac gcc ggc ggc cgg ttc gag tgg gcg ccg      889
100 Val Arg Gly Val Pro Leu Asp Ala Gly Gly Arg Phe Glu Trp Ala Pro
101          240          245          250
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105          255
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111 tgctttttctc tggagctagc aggagcgtag ttattattta gtactacttt acttattcag      1124
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117 aagatctggt ttgtctcaaa aaaaaaaaa aaaaaaaaa aaaaagggcg gccgctctag      1304
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143 Arg Ala Pro Ala Gly Glu Pro Ala Ala Ala Val Ser Ala Gly Gly Asp
144          50          55          60
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148 65          70          75          80
151 Pro Pro Gln Pro Gln Pro Ser Val Asp Ser Val Pro Thr Pro Val Glu
152          85          90          95
155 Ala Ala Asp Gly Ala Ala Gly Gln Gln Gly Ala Ala Leu Ala Ala Gly
156          100         105         110
159 Leu Ser Arg Cys Ser Ser Thr Ala Ser Ser Val Asn Leu Gly Leu Gly
160          115         120         125
163 Gly Gln Arg Gly Ser His Thr Cys Arg Ser Tyr Asp Ala Ala Glu Ala
164          130         135         140
167 Gly Gly Asp His Val Leu Val Asp Val Ser Ala Ala Ser Asn Ser Gly
168 145         150         155         160
171 Ser Gly Pro Asp Arg Glu Arg Arg Glu Thr Thr Pro Ser Ser Arg Ala
172          165         170         175
175 His Gly Glu Leu Ser Asp Leu Glu Ser Asp Leu Ala Gly His Lys Thr
176          180         185         190
179 Gly Pro Ser Leu Pro Ala Ala Thr Pro Ala Ala Glu Leu Ile Val Pro
180          195         200         205
183 Pro Ala His Glu Ile Gln Glu Phe Ala Ala Ala Glu Ala Ala Gln
184          210         215         220
187 Ala Lys Arg Phe Ala Ser Lys Tyr Asn Phe Asp Phe Val Arg Gly Val
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211 tcgaaacctt agcttgccca gccctcccg gcc atg ggc aag tac atg cgc aag      174
212                               Met Gly Lys Tyr Met Arg Lys
213                               1           5
215 gcc aag gct tcc agc gag gtt gtc atc atg gat gtc gcc gcc gct ccg      222
216 Ala Lys Ala Ser Ser Glu Val Val Ile Met Asp Val Ala Ala Ala Pro
217          10          15          20
219 ctc gga gtc cgc acc cga gcg cgc gcc ctc gcg ctg cag cgt ctg cag      270
220 Leu Gly Val Arg Thr Arg Ala Arg Ala Leu Ala Leu Gln Arg Leu Gln
221          25          30          35
223 gag cag cag acg cag tgg gag gaa ggt gct ggc ggc gag tac ctg gag      318

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228 Leu Arg Asn Arg Arg Leu Glu Lys Leu Pro Pro Pro Ala Thr Thr
229 60 65 70
231 agg agg tcg ggc ggg agg aaa gcg gca gcc gag gcc gcc gca act aag 414
232 Arg Arg Ser Gly Gly Arg Lys Ala Ala Ala Glu Ala Ala Ala Thr Lys
233 75 80 85
235 gag gct gag gcg tcg tac ggg gag aac atg ctc gag ttg gag gcc atg 462
236 Glu Ala Glu Ala Ser Tyr Gly Glu Asn Met Leu Glu Leu Glu Ala Met
237 90 95 100
239 gag agg att acc agg gag acg acg cct tgc agc ttg att aac acc cag 510
240 Glu Arg Ile Thr Arg Glu Thr Thr Pro Cys Ser Leu Ile Asn Thr Gln
241 105 110 115
243 atg act agc act cct ggg tcc acg aga tcc agc cac tct tgc cac cgc 558
244 Met Thr Ser Thr Pro Gly Ser Thr Arg Ser Ser His Ser Cys His Arg
245 120 125 130 135
247 agg gtg aac gct cct ccg gtg cac gcc gtc cca agt tcg agg gag atg 606
248 Arg Val Asn Ala Pro Pro Val His Ala Val Pro Ser Ser Arg Glu Met
249 140 145 150
251 aat gag tac ttc gct gcc gaa cag cga cgc caa caa cag gat ttc att 654
252 Asn Glu Tyr Phe Ala Ala Glu Gln Arg Arg Gln Gln Gln Asp Phe Ile
253 155 160 165
255 gac aag tac aac ttc gat cct gca aac gac tgc cct ctc cca ggc agg 702
256 Asp Lys Tyr Asn Phe Asp Pro Ala Asn Asp Cys Pro Leu Pro Gly Arg
257 170 175 180
259 ttt gag tgg gtg aag cta gac tga tggattcaga gggacgagag agcagcaggc 756
260 Phe Glu Trp Val Lys Leu Asp
261 185 190
263 atggaatgga atggaactca ccccccgtc cctccacacc accccagcgt tgtggcagag 816
265 gcgcataccg tcgtgttagc ttctgttctg ctgtaaaaaa aaacttagtg ttttagcatg 876
267 tagccttaat tggtcgtgtg ttacagtaca gaactgatgc tgagttacaa caccctgatc 936
269 tggctcttgat ctgatccctc aactccaatg taacccttaa cagctcattc tgtaaggaac 996
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292 35 40 45
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296 50 55 60
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311 Cys Ser Leu Ile Asn Thr Gln Met Thr Ser Thr Pro Gly Ser Thr Arg
312              115              120              125
315 Ser Ser His Ser Cys His Arg Arg Val Asn Ala Pro Pro Val His Ala
316              130              135              140
319 Val Pro Ser Ser Arg Glu Met Asn Glu Tyr Phe Ala Ala Glu Gln Arg
320 145              150              155              160
323 Arg Gln Gln Gln Asp Phe Ile Asp Lys Tyr Asn Phe Asp Pro Ala Asn
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333 <212> TYPE: DNA
334 <213> ORGANISM: Zea mays
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347 agcgagaaga aggcagtgct gcggcggcgt tccgtaag atg ggg aag tac atg cgc      176
348                               Met Gly Lys Tyr Met Arg
349                               1              5
351 aag cgc agg ggg gcc gcg ggc gag ggg gtg gcc gca gtc gag gtc tcg      224
352 Lys Arg Arg Gly Ala Ala Gly Glu Gly Val Ala Ala Val Glu Val Ser
353              10              15              20
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357              25              30              35
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368 Gly Gly Gly Asp Gly Gly Ser Cys Cys Tyr Ile His Leu Arg Ser Arg
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372 Met Leu Phe Met Ala Ala Pro Gln Gln Gln Pro Ser Ala Ala Leu Thr
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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number

L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6